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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/327,750A

DATE: 02/09/2001

TIME: 14:16:09

Input Set : A:\PTO.txt

Output Set: N:\CRF3\02092001\I327750A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Sato, Taki-Aki
 5 <120> TITLE OF INVENTION: GENE ENCODING NADE, P75NTR- ASSOCIATED CELL DEATH EXECUTOR AND USES
 6 THEREOF
 8 <130> FILE REFERENCE: 0575/59131/JPW/APE
 10 <140> CURRENT APPLICATION NUMBER: 09/327,750A
 11 <141> CURRENT FILING DATE: 1999-06-07
 13 <160> NUMBER OF SEQ ID NOS: 45
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 36
 19 <212> TYPE: DNA
 20 <213> ORGANISM: MOUSE
 22 <400> SEQUENCE: 1
 23 aattgtctac gcataccttat gggggagctg tctaac
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 12
 28 <212> TYPE: PRT
 29 <213> ORGANISM: MOUSE
 31 <400> SEQUENCE: 2
 33 Asn Cys Leu Arg Ile Leu Met Gly Glu Leu Ser Asn
 34 1 5 10
 36 <210> SEQ ID NO: 3
 37 <211> LENGTH: 30
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 W--> 41 <220> FEATURE:
 W--> 41 <223> OTHER INFORMATION: →
 41 <400> SEQUENCE: 3
 42 ctactctagca tcatgtgtgag caaggcgag
 45 <210> SEQ ID NO: 4
 46 <211> LENGTH: 28
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 W--> 50 <220> FEATURE:
 W--> 50 <223> OTHER INFORMATION: →
 50 <400> SEQUENCE: 4
 51 ccgtctgagt cttgtacagc tcttccat
 54 <210> SEQ ID NO: 5
 55 <211> LENGTH: 29
 56 <212> TYPE: DNA
 57 <213> ORGANISM: Artificial Sequence
 W--> 59 <220> FEATURE:
 W--> 59 <223> OTHER INFORMATION: →
 59 <400> SEQUENCE: 5
 60 atcctcgagc gatcatggcc aatgtccac
 63 <210> SEQ ID NO: 6
 64 <211> LENGTH: 27

36

30

Missing Mandatory <220>, <223>
 response to explain source of
 genetic material in the
 artificial sequence. See #12
 on the Error Summary Sheet.

Note: <220> is a mandatory
 blank line feature.

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Input Set : A:\PTO.txt
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65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <400> SEQUENCE: 6
69 atcggatcct ctcagctgta gctccct 27
72 <210> SEQ ID NO: 7
73 <211> LENGTH: 27
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
W--> 77 <220> FEATURE:
W--> 77 <223> OTHER INFORMATION:
77 <400> SEQUENCE: 7
78 atcggatccg atctctctca tctctctc 27
81 <210> SEQ ID NO: 8
82 <211> LENGTH: 27
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
W--> 86 <220> FEATURE:
W--> 86 <223> OTHER INFORMATION:
86 <400> SEQUENCE: 8
87 aaagcttagg gaggcacagc tgagaaa 27
90 <210> SEQ ID NO: 9
91 <211> LENGTH: 27
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
W--> 95 <220> FEATURE:
W--> 95 <223> OTHER INFORMATION:
95 <400> SEQUENCE: 9
96 tttctcagct gtgcctccct aagcttt 27
99 <210> SEQ ID NO: 10
100 <211> LENGTH: 26
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
W--> 104 <220> FEATURE:
W--> 104 <223> OTHER INFORMATION:
104 <400> SEQUENCE: 10
105 atccggagaa aggctaggga ggcaca 26
108 <210> SEQ ID NO: 11
109 <211> LENGTH: 26
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
W--> 113 <220> FEATURE:
W--> 113 <223> OTHER INFORMATION:
113 <400> SEQUENCE: 11
114 tgtgcctccc tagcctttct ccggat 26
117 <210> SEQ ID NO: 12
118 <211> LENGTH: 124
119 <212> TYPE: PRT
120 <213> ORGANISM: MOUSE
122 <400> SEQUENCE: 12

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Error #12
 refer to
 p. 1

RAW SEQUENCE LISTING

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\02092001\I327750A.raw

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124 Met Ala Asn Val His Gln Glu Asn Glu Glu Met Glu Gln Pro Leu Gln
125 1 5 10 15
127 Asn Gly Glu Glu Asp Arg Pro Val Gly Gly Glu Gly His Gln Pro
128 20 25 30
130 Ala Gly Asn Asn Asn Asn Asn Asn His Asn His Asn His Asn His His
131 35 40 45
133 Arg Arg Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg Trp Ala Ile
134 50 55 60
136 Pro Asn Arg Gln Met Asn Asp Gly Leu Gly Gly Asp Gly Asp Asp Met
137 65 70 75 80
139 Glu Met Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys Leu Arg Glu
140 85 90 95
142 Leu Gln Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Glu Leu Ser Asn
143 100 105 110
145 His His Asp His His Asp Glu Phe Cys Leu Met Pro
146 115 120
148 <210> SEQ ID NO: 13
149 <211> LENGTH: 111
150 <212> TYPE: PRT
151 <213> ORGANISM: HUMAN
153 <400> SEQUENCE: 13
155 Met Ala Asn Ile His Gln Glu Asn Glu Glu Met Glu Gln Pro Met Gln
156 1 5 10 15
158 Asn Gly Glu Glu Asp Arg Pro Leu Gly Gly Gly Glu Gly His Gln Pro
159 20 25 30
161 Ala Gly Asn Arg Arg Gly Gln Ala Arg Arg Leu Ala Pro Asn Phe Arg
162 35 40 45
164 Trp Ala Ile Pro Asn Arg Gln Ile Asn Asp Gly Met Gly Gly Asp Gly
165 50 55 60
167 Asp Asp Met Glu Ile Phe Met Glu Glu Met Arg Glu Ile Arg Arg Lys
168 65 70 75 80
170 Leu Arg Glu Leu Gln Leu Arg Asn Cys Leu Arg Ile Leu Met Gly Glu
171 85 90 95
173 Leu Ser Asn His His Asp His His Asp Glu Phe Cys Leu Met Pro
174 100 105 110
176 <210> SEQ ID NO: 14
177 <211> LENGTH: 13
178 <212> TYPE: PRT
179 <213> ORGANISM: cxyzin
181 <400> SEQUENCE: 14
183 Leu Thr Met Lys Glu Val Glu Glu Leu Glu Leu Thr
184 1 5 10
186 <210> SEQ ID NO: 15
187 <211> LENGTH: 13
188 <212> TYPE: PRT
189 <213> ORGANISM: MAPKK
191 <400> SEQUENCE: 15
193 Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
194 1 5 10

```

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PATENT APPLICATION: US/09/327,750A

TIME: 14:16:09

Input Set : A:\PTO.txt

Output Set: N:\CRF3\02092001\I327750A.raw

```

196 <210> SEQ ID NO: 16
197 <211> LENGTH: 10
198 <212> TYPE: PRT
199 <213> ORGANISM: PKI-alpha
201 <400> SEQUENCE: 16
203 Leu Ala Leu Lys Leu Ala Gly Leu Asp Ile
204 1 5 10
206 <210> SEQ ID NO: 17
207 <211> LENGTH: 9
208 <212> TYPE: PRT
209 <213> ORGANISM: TF III A
211 <400> SEQUENCE: 17
213 Leu Pro Val Leu Glu Asn Leu Thr Leu
214 1 5
216 <210> SEQ ID NO: 18
217 <211> LENGTH: 9
218 <212> TYPE: PRT
219 <213> ORGANISM: Rev HIV-1
221 <400> SEQUENCE: 18
223 Leu Pro Pro Leu Glu Arg Leu Thr Leu
224 1 5
226 <210> SEQ ID NO: 19
227 <211> LENGTH: 12
228 <212> TYPE: PRT
229 <213> ORGANISM: Ran BP1
231 <400> SEQUENCE: 19
233 Lys Val Ala Glu Lys Leu Glu Ala Leu Ser Val Arg
234 1 5 10
236 <210> SEQ ID NO: 20
237 <211> LENGTH: 13
238 <212> TYPE: PRT
239 <213> ORGANISM: FMRP
241 <400> SEQUENCE: 20
243 Glu Val Asp Gln Leu Arg Leu Glu Arg Leu Gln Ile Asp
244 1 5 10
246 <210> SEQ ID NO: 21
247 <211> LENGTH: 8
248 <212> TYPE: PRT
249 <213> ORGANISM: Gle 1
251 <400> SEQUENCE: 21
253 Leu Pro Leu Gly Lys Leu Thr Leu
254 1 5
256 <210> SEQ ID NO: 22
257 <211> LENGTH: 14
258 <212> TYPE: PRT
259 <213> ORGANISM: Rex HTLV-1
261 <400> SEQUENCE: 22
263 Ala Leu Ser Ala Gln Leu Tyr Ser Ser Leu Ser Leu Asp Ser
264 1 5 10

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/327,750A

DATE: 02/09/2001
 TIME: 14:16:09

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\02092001\I327750A.raw

```

266 <210> SEQ ID NO: 23
267 <211> LENGTH: 13
268 <212> TYPE: PRT
269 <213> ORGANISM: human NADE
271 <400> SEQUENCE: 23
273 Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln Leu Arg
274 1 5 10
276 <210> SEQ ID NO: 24
277 <211> LENGTH: 13
278 <212> TYPE: PRT
279 <213> ORGANISM: mouse NADE
281 <400> SEQUENCE: 24.
283 Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln Leu Arg
284 1 5 10
286 <210> SEQ ID NO: 25
287 <211> LENGTH: 27
288 <212> TYPE: PRT
289 <213> ORGANISM: MOUSE
291 <400> SEQUENCE: 25
293 Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln Leu Arg Asn Cys Leu
294 1 5 10 15
296 Arg Ile Leu Met Gly Glu Leu Ser Asn His His
297 20 25
299 <210> SEQ ID NO: 26
300 <211> LENGTH: 27
301 <212> TYPE: PRT
302 <213> ORGANISM: HUMAN
304 <400> SEQUENCE: 26
306 Arg Glu Ile Arg Arg Lys Leu Arg Glu Leu Gln Leu Arg Asn Cys Leu
307 1 5 10 15
309 Arg Ile Leu Met Gly Glu Leu Ser Asn His His
310 20 25
312 <210> SEQ ID NO: 27
313 <211> LENGTH: 8
314 <212> TYPE: PRT
315 <213> ORGANISM: CONSENSUS (MOUSE v. HUMAN)
317 <400> SEQUENCE: 27
319 Arg Leu Leu Asn Arg Leu Leu Asn
320 1 5
322 <210> SEQ ID NO: 28
323 <211> LENGTH: 700
324 <212> TYPE: DNA
325 <213> ORGANISM: MOUSE
327 <400> SEQUENCE: 28
328 acgagcgtct ggcacgacgc tcggagctcc tctgcgcgcg gggggctggc agcgggcccc 60
330 aggcgagcgg gacagattga ctggaagccg agagtcacgg cggcagcggg aattgacagg 120
332 aggactacgc cgcaagggat aggccacagaa tagcaaccag gaaacaaaat ctcacatcgg 180
334 ccaatgtcca ccaggaaaac gaagagctgg agcagccctt gcagaatgga caggaacacc 240
336 gccctgtggg aggaggtgag ggcaccagc ctgctgcaaa caacaacaac aacaaccaca 300

```

VERIFICATION SUMMARY

DATE: 02/09/2001

PATENT APPLICATION: US/09/327,750A

TIME: 14:16:10

Input Set : A:\PTO.txt

Output Set: N:\CRF3\02092001\I327750A.raw

L:41 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:41 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:50 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:50 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:59 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:59 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:77 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:77 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:86 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:86 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:95 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:95 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:104 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:104 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:113 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:113 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/327,750A

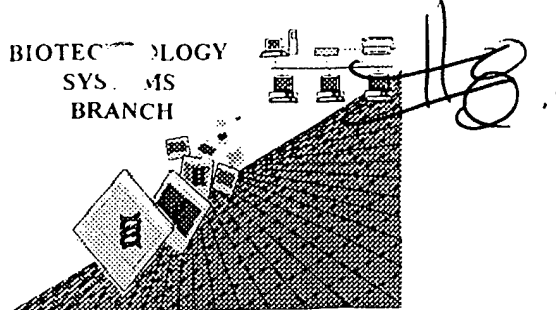
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ³⁻¹¹ ☒ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

J. Kerr

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/327,750 A

Source: 1633

Date Processed by STIC: 2-9-01

RECEIVED

MAR 01 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>